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Domains in membranes with active two-state inclusions

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The distribution of inclusion-rich domains in membranes with active two-state inclusions is studied by simulations. The purpose of this study is to check whether the conformation changes of membrane-bound proteins can actively control the size of protein-rich domains in biomembranes. A Monte Carlo simulation which neglects the effect of solvent dynamics and the active forces of the proteins is applied to the simulations.

The main results of our simulations in the study of finite-size domains in biomembranes are: (a) Small domains with only several inclusions are observed for inclusions with time scales($\sim 10^{-3}$ s) and interaction energy (kBT) comparable to motor proteins, i.e., our simple model is able to produce the kind of small inclusion clusters observed in within typical parameter range. (b) Typical size of inclusion-rich domain (L) scales as $L \sim k_{21}^{-1/3}$. This often observed behavior provides a mechanism to control continuously the size of inclusion-rich domains by inclusion activities. (c) A switch-like response of typical size of inclusion-rich domains to the external stimuli is found at fixed k_{21}: There exists a crossover transition rate k_{12}^* such that L depends weakly on the stimuli (k_{12}) when $k_{12} < k_{12}^*$ but becomes very sensitive to it (i.e., L increases rapidly as k_{12} increases) when $k_{12} > k_{12}^*$. The crossover k_{12}^* occurs when the diffusion length of a state-2 inclusion within its lifetime is about the same as L. Notice that a similar switch-like behavior is observed in experiment. (d) L decreases when the coupling between state-1 inclusion and membrane curvature increases.

Although our model has neglected hydrodynamics of the solvent and active forces exerted by the inclusions, the mechanism proposed in the current study is rather general and should exist in models which take these effects into account.

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